

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:30 ; Search time 8498.8 Seconds
(without alignments)
32.874 Million cell updates/sec

Title: US-09-851-670-18

Perfect score: 26
Sequence: 1 ttatgtgacatcttgcacgat 26

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 11351937 seqs, 5372869281 residues

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estopl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hnc:*
10: gb_est1:*
11: gb_est2:*
12: gb_hnc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rnd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	57.7	59	10	AL593945
2	14.8	56.9	52	10	BE322167
3	14.6	56.2	52	13	A2647203
4	14.4	55.4	46	13	AQ025201
5	14.4	55.4	55	10	A1920251
6	14	53.8	52	10	AA935402
7	13.8	53.1	29	10	AA250048
8	13.6	52.3	59	11	T61794
9	13.4	51.5	31	10	A1973656
10	13.4	51.5	33	13	A2760071
11	13.4	51.5	46	10	AA232414
12	13.4	51.5	55	10	AA288258

c 13	13.4	51.5	55	10	AA566958
c 14	13.4	51.5	60	10	BE317966
c 15	13.2	50.8	44	10	AM355214
c 16	13.2	50.8	44	13	A2778327
c 17	13.2	50.8	52	11	H28465
c 18	13.2	50.8	55	11	T70039
c 19	13.2	50.8	58	10	A1959431
c 20	13	50.0	23	13	TA266D020
c 21	13	50.0	55	10	AA754857
c 22	13	50.0	56	11	BE638275
c 23	13	50.0	60	11	H55533
c 24	12.8	49.2	42	11	D67715
c 25	12.8	49.2	43	11	AT085127
c 26	12.8	49.2	43	11	WA11103
c 27	12.8	49.2	50	10	AA999944
c 28	12.8	49.2	51	13	BH011434
c 29	12.8	49.2	55	10	AA142590
c 30	12.8	49.2	55	13	A2775247
c 31	12.8	49.2	57	13	A2454242
c 32	12.8	49.2	58	10	AA792062
c 33	12.8	49.2	58	10	AT707554
c 34	12.8	49.2	58	10	AT707742
c 35	12.8	49.2	58	11	N92878
c 36	12.8	49.2	59	13	A2813936
c 37	12.8	49.2	60	11	BT082549
c 38	12.6	48.5	23	13	A2316806
c 39	12.6	48.5	27	13	A2838052
c 40	12.6	48.5	38	11	D18219
c 41	12.6	48.5	40	10	A1140952
c 42	12.6	48.5	50	10	AU104339
c 43	12.6	48.5	50	10	AU104340
c 44	12.6	48.5	50	10	AU104344
c 45	12.6	48.5	50	10	AU104352

ALIGNMENTS

RESULT 1
AL593945 59 bp mRNA
LOCUS AL593945 XGC-gastrula silurana tropicalis cDNA clone TGA004c16 5',
DEFINITION mRNA sequence.
ACCESSION AL593945.1 GI:15006006
VERSION
KEYWORDS
SOURCE
ORGANISM
western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 59)
Huckle, E., Taylor, R., McMurray, A., Ashurst, J.L., Zorn, A.M. and
Rogers, J.

REFERENCE
AUTHORS
Sanger Xenopus tropicalis EST project 2001
TITLE
JOURNAL
COMMENT
Unpublished (2001)
Contact: Huckie E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPHICALIS_SEQUENCE_ID: TGA004c16.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1..59
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGA004c16"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli DH10B"

FEATURES

source

```

/NOTE=Vector: PCS107; Site.1: EcoRI; Site.2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into PCS107 with EcoRI at the 5' end and NotI at the 3'
end."

```

Query Match	57.7%	Score 15;	DB 10;	Length 59;
Best Local Similarity	78.3%;	Pred. No. 2.6e+04;		
Matches 18; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0

```
Qy 1 tcatgtggccatcttgtccag 23
    ||| | | ||||| |||
Db 28 TTAGTCTTGCCATCTTTACCAg 6
```

RESULT	2		
BE322167			
LOCUS	BE322167	52 bp	MRNA
DEFINITION	NEF010G05IN1E1037 Insect herbivory Medicago truncatula cDNA clone	EST	21-DEC-2000
ACCESSION	BE322167		
VERSION	BE322167		
KEYWORDS	BE322167.2	GI:11964189	
SOURCE	EST.		
ORGANISM	barrel medic.		
	Medicago truncatula		

REFERENCE	1 (bases 1 to 52)
AUTHORS	North,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
TITLE	,H.R., Imman,J.T., Weller,J.W. and May,G.D.
JOURNAL	Expressed Sequence Tags from the Samuel Roberts Noble Foundation
COMMENT	Medicago truncatula insect herbivory library
	(unpublished 2000)
	On Jul. 10, 2000, this sequence version replaced gi:9195944.

217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Tel: 501 575 5191
Fax: 501 575 7601
Email: khorlthcomp.uark.edu
Medicago Genome Initiative accession: MGI:S:23992
Insert Length: 659 Std Error: 0.00
Plate: 010 row: G column: 05
Seq primer: TCACACAGGAACACACTGTGAC.

```

FEATURES
source
location/Qualifiers
1..52
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF0106051N"
/clone_lib="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
damaged leaves from injured plants) and wounded leaves
were harvested and pooled."
BASE COUNT
11 a 17 c 3 g 21 t

```

Query Match	56.9%	Score 14.8	DB 10	Length 52
Best Local Similarity	73.1%	Pred. No. 3.1e+04		
Matches 19, Conservative	0	Mismatches 7	Indels 0	Gaps 0

QY 1 ttattgtgccatcttgtccagcat 26
|| || | ||||| || |||||

Db 23 TTCTTCTCTTCATCTTTTCTCAAGCAT 48

RESULT

LOCUS	AZ647203	52 bp	DNA	GSS	14-DEC-2000
DEFINITION	IM0513004R Mouse 10kb plasmid UUGC1M library. Mus musculus genomic clone UUGC1M0513004 R, DNA sequence.				

VERSION	AZ647203.1	GI:11778434
KEYWORDS	GSS.	
SOURCE	house mouse.	

ORGANISM

REFERENCES
AUTHORS

TITLE

JOURNAL
COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

```
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.000
Plate: 0513 row: 0 column: 04
Seq primer: CACACACGGAACACGTATGCC
Class: plasmid ends
High quality sequence stop: 52.
```

FEATURES	Location/Qualifiers
source	1. .52

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0513004"
/clone_id="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD24ny: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource"

```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[bp]AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT	21 a	13 c	8 g	10 t
ORIGIN				

Query Match	56.28;	Score	14.6;	DB	13;	Length	52;
Best Local Similarity	81.08;	Pred. No.	3.7e+04;				
Matches	17;	Conservative	0;	Mismatches	4;	Indels	0;
						Gaps	0;

QY 1 ttattgtgcatcttgtcc 21

Db 33 TTATGCTGCTCCTGTC 13

RESULT 4
AQ025201

LOCUS
DEFINITION

DEFINITION EP(3)1219 *Drosophila melanogaster* EP line *Drosophila melanogaster* genomic Sequence recovered from 5' end of P element, DNA sequence

ACCESSION	AQ025201
VERSION	AQ025201.1
REVISION	GI:3265553

KEYWORDS

SOURCE

ORGANISM

CONCLUSIONS

REFERENCE

AUTHORS
TITLE

1

JOURNAL
MEDLINE

COMMENT

Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.

The P element insertion position is base 39 in the 46 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

FEATURES

Source

/organ
/dh yr

```
clone lib="Drosophila melanogaster
```

```
/note="Inverse PCR wa
```

melanogaster strains each of which contains a

transposable element insertion'. (The generation

resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfully.berkeley.edu/p-disrupt/inverse_pcr.html.

BASE COUNT
ORIGIN

Query Match

Best Local Similarity 75.0%; pred. No. 4.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels

QY. 1

19 05

RESULT

AI920251/0
LOGIC

LOCUS

DEFINITION

VERSION AI920251.1 GI:5649883

KEYWORD

SOURCE

ORGAN

REFERENCES

WELBORN
AUTHOR

TITLE

JOURN

Trace considered overall poor quality
Seq primer: 40m13 fwd. ET from AmerSham
High quality sequence stop: 1.

FEATURES

source

1. .52

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1459637"

/clone_lib="NCI-CGAP_K1d6"

/sex="mixed"

/tissue_type="Kidney tumor"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: Kidney; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCAGCAG 3' 3' adaptor sequence: 5'
CTCAGATTTTATTTTATTTTATTTT 3' Average insert size: 1.0 kb."

BASE COUNT

19 a 8 c 11 g 14 t

ORIGIN

3 a 6 c 2 g 18 t

Query Match

Best Local Similarity 53.8%; Score 14; DB 10; Length 52;
77.3%; Pred. No. 6.6e+04;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 tttgtggcattcttgcacagat 26

Db 50 TATGACTATCTTGTCCATTAT 29

RESULT 7

AM250048

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .29

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2819281"

Location/Qualifiers

1. .29

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2819281"

Location/Qualifiers

1. .29

/organism="Homo sapiens"

/clone_lib="NIH_MGC-7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dt priming. Directionally
cloned into EORI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

3 a 6 c 2 g 18 t

Query Match

Best Local Similarity 53.1%; Score 13.8; DB 10; Length 29;
72.0%; Pred. No. 7.7e+04;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 tttatgtggcattcttgcacaga 25

Db 4 TTTTGTGCTTCTTTTCCACCA 28

RESULT 8

T61794

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .59

/organism="Homo sapiens"

/db_xref="GDB:498695"

/clone="IMAGE:78950"

/clone_lib="Stratagene Liver (#937224)"

/sex="male"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: Liver; Vector: pBluescript SK-; Site_1: EORI

Location/Qualifiers

1. .59

/organism="Homo sapiens"

/db_xref="GDB:498695"

/clone="IMAGE:78950"

/clone_lib="Stratagene Liver (#937224)"

/clone_lib="NIH_MGC-7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dt priming. Directionally
cloned into EORI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

3 a 6 c 2 g 18 t

Query Match

Best Local Similarity 53.1%; Score 13.8; DB 10; Length 29;
72.0%; Pred. No. 7.7e+04;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 tttatgtggcattcttgcacaga 25

Db 4 TTTTGTGCTTCTTTTCCACCA 28

RESULT 8

T61794

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .59

/organism="Homo sapiens"

/db_xref="GDB:498695"

/clone="IMAGE:78950"

/clone_lib="Stratagene Liver (#937224)"

/sex="male"

/dev_stage="49 years old"

/lab_host="SOLR cells (kanamycin resistant)"

/note="Organ: Liver; Vector: pBluescript SK-; Site_1: EORI

Location/Qualifiers

1. .59

/organism="Homo sapiens"

/db_xref="GDB:498695"

/clone="IMAGE:78950"

/clone_lib="Stratagene Liver (#937224)"

BASE COUNT
ORIGIN
11 a 20 c 16 g 11 t 1 others
Site 2: XhoI: Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb. Uni-ZAP XR Vector: ~5' adaptor sequence: 5' GAATTCGCGACGAC 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

[illegible]

RESULT	9
LOCUS	A1973656
DEFINITION	A1973656 31 bp mRNA EST 25-AUG-1999
ACCESSION	sdd07hl.y1 Gm-cl020 Glycine max CDNA clone GENOME SYSTEMS CLONE ID
VERSION	Gm-cl020-1054 5' similar to SW:NO51_SOYBN P04671 NODULIN C51. ;
KEYWORDS	mRNA sequence.
SOURCE	A1973656
EST	A1973656.1 GI:5770482
	soybean.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 31)				
	Shoemaker, R., Keim, P., Vothin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, R., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.	Public Soybean EST Project	Unpublished (1999)	Contact: Shoemaker R/Public soybean EST project.

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Trace considered overall poor quality
Sed primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .31

```

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl020-1054"
/clone_lib="Gm-cl020"
/tissue_type="root modules of greenhouse grown plants"
/lab_host="XL10-Gold"
/notes="Vector: pBluescript II SK+; Site.1: EcoRI; Site.2:
XhoI; This cDNA library was constructed from mRNA isolated
from nodules on the roots of 2.5 month-old Glycine max
'Williams' plants that were greenhouse grown. The cDNA
library was prepared using the Stratagene pBluescript II
SK(+)' library construction kit. First strand synthesis was
performed with 5-methyl dCTP, hence the ligated cDNA was
hememethylated. A modification of Stratagene's

```

first-strand synthesis primer was used. An 'anchor' nucleotide (v-A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGACTGACCTGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase and size-fractionated with a 400 bp cutoff, using a SizeSep 400 Spin column from Pharmacia. The column eluent was ligated to EcoRI adaptors and phosphorylated. The XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA size Predicted vector (pNucScript II SK+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-55) and sequence (n-16). This library was constructed by Dr. Paul Kelm and Dr. Virginia Coryell.

Query Match	51.5%;	Score 13.4;	DB 10;	Length 31;
Best Local Similarity	73.9%;	Pred. No. 1.1e+05;		
Matches 17;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
OY	3	atgtgscacattgtgccagaa	25	
db	9	ATGTGCCCCACTTTATCAACA	31	

	AZ760071	RESULT 10
	AZ760071	LOCUS
	AZ760071	DEFINITION
	IM055JC03R Mouse 10kb plasmid UUGC1M library	GSS
	C10E.UUCG1M055JC03 R, DNA sequence.	Mus musculus genomic
	AZ760071	ACCESSION
	AZ760071.1 GI:12867513	VERSION
	GGB.	KEYWORDS
SOURCE	house mouse,	
ORGANISM	Mus musculus	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 33)	Maimoud, E., Luvina, I., Kocentka, S., Chodogian, P., Maline, M., Maline, P.,	Mouse whole genome scaffolding with paired end reads from 10kb	Unpublished (2000)	Contact: Robert B. Weiss
2	Dunn, D., Longacre, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,	Plasmid inserts		
3	Islam, H., Aoyagi, A., S., Maimoud, M., Meenen, E., Petersen, T., Kelly			
4	, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.			
5	and Wright, D., Weiss, R.			

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0553 row: C column: 03
Seq primer: CACACAGCAAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. .33

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="UMC1M0553C03"
/clone_lib="Mouse 10kb plasmid UMC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

```

```
/organism="Homo sapiens"  
/db_xref="GDB:5426137"  
/db_xref="taxon:9606"  
/clone="IMAGE:664207"  
/clone_lib="Stratagene NM2 neuronal precursor 937230"
```

(note=vector: pT73/pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTCACATCGAGCTGGGACGCCGCCGTCTTTTCTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bettarid Jordan. Library went through three rounds of normalization, and was constructed by

Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu.
Location/Qualifiers

FEATURES
Source

1. .44
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pnf-b.pk0001.a6"
/clone_lib="chicken fat cDNA library pBSII"
/sex="Male and Female"
/tissue_type="fat"
/lab_host="E.coli DH10B"
/note="Vector: pBSII"

BASE COUNT 21 a 6 c 3 g 14 t
ORIGIN

Query Match 50.8%; Score 13.2; DB 10; Length 44;
Best Local Similarity 69.2%; Pred. No. 1.4e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 ttattgtggccatctttgtccagcat 26
||||||| | ||| | |||||
Db 28 TTATTGTTAATTTTATTATACAGCAP 3

Search completed: March 9, 2002, 00:09:32
Job time: 11048 sec